



5-3-01.

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:	09/828,317
••	
Source:	OIPE
	•
Date Processed by STIC:	4-23-01

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 c-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 c-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/828, 3/7 ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE 1 ____ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces. Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers. Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed. Variable Length Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid Patentin ver. 2.0 "bug" ... Normally, Patentin would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. Skipped Sequences _ missing. If intentional, please use the following format for each skipped sequence: Seguence(s) _ (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). Skipped Sequences Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence, (NEW RULES) <210> sequence id number <400> sequence id number 000 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. (NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. (NEW RULES) Valid response is Artificial Sequence. Use of <220>Feature Sequence(s) ___ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules) Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted PatentIn ver. 2.0 "bug"

AMC - Biotechnology Systems Branch - 4/06/2001

file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).

Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

DATE: 04/23/2001 RAW SEQUENCE LISTING PATENT APPLICATION: US/09/828,317 TIME: 13:14:04

Input Set : A:\20620Y SEQLIST.TXT

Output Set: N:\CRF3\04232001\1828317.raw

Does Not Comply Corrected Diskette Needed

See pp. 1-5 4 <110> APPLICANT: Merck & Co., Inc. Craig A. Stump Theresa M. Williams 8 <120> TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE 11 <130> FILE REFERENCE: 20620Y C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/828,317 C--> 13 <141> CURRENT FILING DATE: 2001-04-06 13 <150> PRIOR APPLICATION NUMBER: 60/195,802 14 <151> PRIOR FILING DATE: 2000-04-10 16 <160> NUMBER OF SEQ ID NOS: 25 18 <170> SOFTWARE: FastSEQ for Windows Version 4.0 20 <210> SEQ ID NO: 1 21 <211> LENGTH: 4 22 <212> TYPE: PRT 23 <213> ORGANISM: Artificial Sequence 25 <220> FEATURE: 26 <223> OTHER INFORMATION: N-terminus of Ras protein 28 <400> SEQUENCE: 1 29 Cys Val Leu Leu 30 1 32 <210> SEQ ID NO: 2 33 <211> LENGTH: 4 34 <212> TYPE: PRT 35 <213> ORGANISM: Artificial Sequence 37 <220> FEATURE: 38 <223> OTHER INFORMATION: N-terminus of Ras protein 40 <400> SEQUENCE: 2 41 Cys Val Leu Ser Circled responses for the source of the 42 1 44 <210> SEQ ID NO: 3 45 <211> LENGTH: 15 46 <212> TYPE: PRT 47 <213> ORGANISM: Artificial Sequence artificial sequences 49 <220> FEATURE: 50 <223> OTHER INFORMATION: Completely Synthetic Amino Acid 52 <400> SEQUENCE: 3 53 Gly Lys Lys Lys Lys Lys Ser Lys Thr Lys Cys Val Ile Met need to be more 54 1 precise as to the type 56 <210> SEQ ID NO: 4 57 <211> LENGTH: 52 of sequence, or the 58 <212> TYPE: DNA 59 <213> ORGANISM: Artificial Sequence genetic material making 61 <220> FEATURE: 62 <223> OTHER INFORMATION: Artificial Nucleotide Sequence up the 52 sequence. 64 <400> SEQUENCE: 4 65 gagagggaat tegggeeett eetgeatget getgetgetg etgetgetgg ge See #12 on the Error 67 <210> SEQ ID NO: 5 Summery sheet.





Input Set : A:\20620Y SEQLIST.TXT
Output Set: N:\CRF3\04232001\I828317.raw

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Input Set : A:\20620Y SEQLIST.TXT
Output Set: N:\CRF3\04232001\1828317.raw

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Input Set : A:\20620Y SEQLIST.TXT
Output Set: N:\CRF3\04232001\1828317.raw

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Input Set : A:\20620Y SEQLIST.TXT
Output Set: N:\CRF3\04232001\I828317.raw

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VERIFICATION SUMMARYDATE: 04/23/2001PATENT APPLICATION: US/09/828,317TIME: 13:14:05

Input Set : A:\20620Y SEQLIST.TXT
Output Set: N:\CRF3\04232001\1828317.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date